



# SEQUENCE LISTING

<110> Denney, Jr., Dan W.  
<120> Vaccines for Treatment of Lymphoma and Leukemia  
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<140> 09/370,453  
<141> 1999-08-09  
<160> 77  
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Ser	Pro	Lys	Met	Val	Lys	Val	Ala	Ser	Leu	Leu	Val	Lys	Arg	Thr	Ser		
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Arg Ser Val Gly Tyr Arg Pro Asp Phe Val Gly Phe Glu Ile Pro Asp	
170 175 180 185	

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Lys Phe Val Val Gly Tyr Ala Leu Asp Tyr Asn Glu Tyr Phe Arg Asn	
190 195 200	

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Leu Asn His Val Cys Val Ile Ser Glu Thr Gly Lys Ala Lys Tyr Lys	
205 210 215	

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Tyr Ile Lys Ala Leu Asn Arg Asn Ser Asp Arg Ser Ile Pro Met Thr  
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Val Asp Phe Ile Arg Leu Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly  
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Asp Ile Lys Val Ile Gly Gly Asp Asp Leu Ser Thr Leu Thr Gly Lys  
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Thr Leu Leu Ser Leu Val Lys Gln Tyr Ser Pro Lys Met Val Lys Val  
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Ala Ser Leu Leu Val Lys Arg Thr Ser Arg Ser Val Gly Tyr Arg Pro  
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Asp Phe Val Gly Phe Glu Ile Pro Asp Lys Phe Val Val Gly Tyr Ala  
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Asn Glu Phe Lys Tyr Phe Gln Arg Met Thr Thr Thr Ser Ser Val Glu
30 35 40 45

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Gly Lys Gln Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile
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cct gag aag aat cga cct tta aag gac aga att aat ata gtt ctc agt 243
Pro Glu Lys Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser
65 70 75

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 Leu Asp Asp Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys  
 95 100 105  
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 Val Asp Met Val Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala  
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 Met Asn Gln Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln  
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 175 180 185  
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Lys Tyr Phe Gln Arg Met Thr Thr Thr Ser Ser Val Glu Gly Lys Gln  
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Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser Arg Glu Leu  
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Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser Leu Asp Asp  
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Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys Val Asp Met  
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Val Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala Met Asn Gln  
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ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc 96  
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 Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met  
 35 40 45

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 50 55 60

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 Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu  
 65 70 75 80

gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa 288  
 Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu  
 85 90 95

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 Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro  
 100 105 110

gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac 384  
 Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn  
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Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr	
145 150 155 160	
gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc	528
Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu	
165 170 175	
ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac	576
Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His	
180 185 190	
tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca	624
Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro	
195 200 205	
agc cct ctc cca aat aaa gga agt gga acc act tca ggt act acc cgt	672
Ser Pro Leu Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg	
210 215 220	
ctt cta tct ggg cac acg tgt ttc acg ttg aca ggt ttg ctt ggg acg	720
Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr	
225 230 235 240	
cta gta acc atg ggc ttg ctg act tag	747
Leu Val Thr Met Gly Leu Leu Thr	
245	

<210> 27  
 <211> 248  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 27

Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val	
1 5 10 15	
Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile	
20 25 30	
Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met	
35 40 45	
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys	
50 55 60	

Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu  
65 70 75 80

Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu  
85 90 95

Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro  
100 105 110

Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn  
115 120 125

Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val  
130 135 140

Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr  
145 150 155 160

Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu  
165 170 175

Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His  
180 185 190

Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro  
195 200 205

Ser Pro Leu Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg  
210 215 220

Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr  
225 230 235 240

Leu Val Thr Met Gly Leu Leu Thr  
245

<210> 28  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 28  
ccacttcctt tatttggtgc agattcag

28

<210> 29  
 <211> 786  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<220>  
 <221> CDS  
 <222> (1)..(783)

<400> 29  
 atg gtg tgt ctg aag ctc cct gga ggc tcc tgc atg aca gcg ctg aca 48  
 Met Val Cys Leu Lys Leu Pro Gly Gly Ser Cys Met Thr Ala Leu Thr  
 1 5 10 15  
 gtg aca ctg atg gtg ctg agc tcc cga ctg gct ttg gct ggg gac acc 96  
 Val Thr Leu Met Val Leu Ser Ser Arg Leu Ala Leu Ala Gly Asp Thr  
 20 25 30  
 cga cca cgt ttc ttg tgg cag ctt aag ttt gaa tgt cat ttc ttc aat 144  
 Arg Pro Arg Phe Leu Trp Gln Leu Lys Phe Glu Cys His Phe Phe Asn  
 35 40 45  
 ggg acg gag cgg gtg cgg ttg ctg gaa aga tgc atc tat aac caa gag 192  
 Gly Thr Glu Arg Val Arg Leu Leu Glu Arg Cys Ile Tyr Asn Gln Glu  
 50 55 60  
 gag tcc gtg cgc ttc gac agc gac gtg ggg gag tac cgg gcg gtt gag 240  
 Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Glu  
 65 70 75 80  
 gag ctg ggg cgg cct gat gcc gag tac tgg aac agc cag aag gac ctc 288  
 Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu  
 85 90 95  
 ctg gag cag aag cgg ggc cag gtg gac aat tac tgc aga cac aac tac 336  
 Leu Glu Gln Lys Arg Gly Gln Val Asp Asn Tyr Cys Arg His Asn Tyr  
 100 105 110  
 ggg gtt ggt gag agc ttc aca gtg cag cgg cga gtt gag cct aag gtg 384  
 Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Glu Pro Lys Val  
 115 120 125  
 act gtg tat cct tca aag acc cag ccc ctg cag cac cac aac ctc ctg 432  
 Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu  
 130 135 140  
 gtc tgc tct gtg agt ggt ttc tat cca ggc agc att gaa gtc agg tgg 480  
 Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp  
 145 150 155 160  
 ttc cgg aac ggc cag gaa gag aag gct ggg gtg gtg tcc acg ggc ctg 528  
 Phe Arg Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu  
 165 170 175



atc	cag	aat	gga	gat	tgg	acc	ttc	cag	acc	ctg	gtg	atg	ctg	gaa	ata	576
Ile	Gln	Asn	Gly	Asp	Trp	Thr	Phe	Gln	Thr	Leu	Val	Met	Leu	Glu	Ile	
			180					185					190			

gtt	cct	cgg	agt	gga	gag	gtt	tac	acc	tgc	caa	gtg	gag	cac	cca	agt	624
Val	Pro	Arg	Ser	Gly	Glu	Val	Tyr	Thr	Cys	Gln	Val	Glu	His	Pro	Ser	
		195					200					205				

gtg	acg	agc	cct	ctc	aca	gtg	gaa	tgg	aga	gca	cgg	tct	gaa	tct	gca	672
Val	Thr	Ser	Pro	Leu	Thr	Val	Glu	Trp	Arg	Ala	Arg	Ser	Glu	Ser	Ala	
	210					215					220					

cca	aat	aaa	gga	agt	gga	acc	act	tca	ggt	act	acc	cgt	ctt	cta	tct	720
Pro	Asn	Lys	Gly	Ser	Gly	Thr	Thr	Ser	Gly	Thr	Thr	Arg	Leu	Leu	Ser	
225					230					235					240	

ggg	cac	acg	tgt	ttc	acg	ttg	aca	ggt	ttg	ctt	ggg	acg	cta	gta	acc	768
Gly	His	Thr	Cys	Phe	Thr	Leu	Thr	Gly	Leu	Leu	Gly	Thr	Leu	Val	Thr	
				245					250					255		

atg	ggc	ttg	ctg	act	tag											786
Met	Gly	Leu	Leu	Thr												
			260													

<210> 30  
 <211> 261  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 30

Met	Val	Cys	Leu	Lys	Leu	Pro	Gly	Gly	Ser	Cys	Met	Thr	Ala	Leu	Thr
1				5					10					15	

Val	Thr	Leu	Met	Val	Leu	Ser	Ser	Arg	Leu	Ala	Leu	Ala	Gly	Asp	Thr
			20					25					30		

Arg	Pro	Arg	Phe	Leu	Trp	Gln	Leu	Lys	Phe	Glu	Cys	His	Phe	Phe	Asn
		35					40					45			

Gly	Thr	Glu	Arg	Val	Arg	Leu	Leu	Glu	Arg	Cys	Ile	Tyr	Asn	Gln	Glu
	50					55					60				

Glu	Ser	Val	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Glu
65					70					75					80

Glu	Leu	Gly	Arg	Pro	Asp	Ala	Glu	Tyr	Trp	Asn	Ser	Gln	Lys	Asp	Leu
				85					90					95	

Leu Glu Gln Lys Arg Gly Gln Val Asp Asn Tyr Cys Arg His Asn Tyr  
100 105 110

Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Glu Pro Lys Val  
115 120 125

Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu  
130 135 140

Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp  
145 150 155 160

Phe Arg Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu  
165 170 175

Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Ile  
180 185 190

Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser  
195 200 205

Val Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala  
210 215 220

Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser  
225 230 235 240

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr  
245 250 255

Met Gly Leu Leu Thr  
260

<210> 31  
 <211> 189  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<220>  
 <221> CDS  
 <222> (1)..(186)

<400> 31  
 ttg gat cca cga tcg ttt cta ttg cgc aat cca aat gat aag tac gaa 48  
 Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu  
 1 5 10 15  
 cca ttt tgg gaa gat act aca gag aac gtg gtg tgt gcc ctg ggc ctg 96  
 Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu  
 20 25 30  
 act gtg ggt ctg gtg ggc atc att att ggg acc atc ttc atc atc aag 144  
 Thr Val Gly Leu Val Gly Ile Ile Ile Gly Thr Ile Phe Ile Ile Lys  
 35 40 45  
 gga gtg cgc aaa agc aat gca gca gaa cgc agg ggg cct ctg taa 189  
 Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu  
 50 55 60

<210> 32  
 <211> 62  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 32  
 Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu  
 1 5 10 15  
 Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu  
 20 25 30  
 Thr Val Gly Leu Val Gly Ile Ile Ile Gly Thr Ile Phe Ile Ile Lys  
 35 40 45  
 Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu  
 50 55 60

<210> 33  
 <211> 192  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<220>  
 <221> CDS  
 <222> (1)..(189)

<400> 33  
 ttg gat cca cga tcg ttt cta ttg cgc aat cca aat gat aag tac gaa 48  
 Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu  
 1 5 10 15  
 cca ttt tgg gaa gat cag agc aag atg ctg agt gga gtc ggg ggc ttc 96  
 Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe  
 20 25 30  
 gtg ctg ggc ctg ctc ttc ctt ggg gcc ggg ctg ttc atc tac ttc agg 144  
 Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg  
 35 40 45  
 aat cag aaa gga cac tct gga ctt cag cca aca gga ttc ctg agc tga 192  
 Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser  
 50 55 60

<210> 34  
 <211> 63  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 34  
 Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu  
 1 5 10 15  
 Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe  
 20 25 30  
 Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg  
 35 40 45  
 Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser  
 50 55 60

<210> 35  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic  
  
 <400> 35  
 cgatcgtgga tccaagttta gggtcgtatc tgtttcaaa 39  
  
 <210> 36  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic  
  
 <400> 36  
 cgatcgagga tccaagatgg tggcagacag gacc 34  
  
 <210> 37  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic  
  
 <400> 37  
 acgcgtccac catggccata agtggagtcc ct 32  
  
 <210> 38  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic  
  
 <400> 38  
 ggatccaact ctgtagtctc tgggagag 28

<210> 39  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic  
  
 <400> 39  
 acgcgtccac catggtgtgt ctgaagctcc tg 32

<210> 40  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic  
  
 <400> 40  
 ggatccaact tgctctgtgc agattcaga 29

<210> 41  
 <211> 292  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 41  
 gaattctttt ttgcgtgtgg cagttttaag ttattagttt ttaaaatcag tacttttttaa 60  
 tggaacaac ttgacaaaa atttgtcaca gaattttgag acccattaaa aaagttaaat 120  
 gagaaacctg tgtgttcctt tggtaaacac cgagacattt aggtgaaaga catctaattc 180  
 tggttttacg aatctggaaa cttcttgaaa atgtaattct tgagttaaca cttctgggtg 240  
 gagaataggg ttgttttccc cccacataat tggaagggga aggaatatcg at 292

<210> 42  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic  
  
 <400> 42  
 tcgatggcgc gccttaatta 20

<210> 43  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 43  
 agcttaatta aggcgcgcca 20

<210> 44  
 <211> 1147  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 44  
 gcggccgcgt cgaccaaggg ccccgagcgtg ttccccctgg cccctgctc ccgcagcacc 60  
 agcggcgcca ccgccgccct gggctgcctg gtgaaggact acttccccga gcccgtagacc 120  
 gtgagctgga acagcggcgc cctgaccagc ggcgccaca ccttccccgc cgtgctgcag 180  
 tccagcggcc tgtactccct gagcagcgtg gtgaccgtgc ccagcagcag cctgggcacc 240  
 cagacctaca cctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagcgcgtg 300  
 gagctgaaga cccccctggg cgacaccacc cacacctgcc cccgctgccc cgagcccaag 360  
 agctgcgaca cccctcccc ctgccccgc tgccccgagc ccaagagctg cgacaccct 420  
 cccccctgcc cccgctgccc cgagcccaag agctgcgaca cccctcccc ctgccccgc 480  
 tgccccgccc ccgagctgct gggcgcccc agcgtgttcc tgttcccccc caagcccaag 540  
 gacacctga tgatctcccg ccccccgag gtgacctgcg tgggtggtgga cgtgagccac 600  
 gaggaccccc aggtgcagtt caagtgttac gtggacggcg tggaggtgca taacgccaaag 660  
 accaagcccc gcgaggagca gtacaacagc accttccgcg tggtagcgt gctgaccgtg 720  
 ctgcaccagg actggctgaa cggcaaggag tacaagtga aggtgagcaa caaggccctg 780  
 cccgccccca tcgagaagac catctccaag accaagggcc agccccgga gccccaggtg 840  
 tacacctgc cccccagccg cgaggagatg accaagaacc aggtgagcct gacctgcctg 900  
 gtgaagggct tctacccccag cgacatcgcc gtggagtggg agagcagcgg ccagccccgag 960  
 aacaactaca acaccacccc ccccatgctg gacagcgacg gcagcttctt cctgtacagc 1020  
 aagctgaccg tggacaagag ccgctggcag cagggcaaca tcttctctg cagcgtgatg 1080

catgaggccc tgcacaaccg cttcacccag aagagcctga gcctgagccc cggcaagtga 1140  
tagatct 1147

<210> 45  
<211> 377  
<212> PRT  
<213> Homo sapiens

<400> 45

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
65 70 75 80

Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
85 90 95

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro  
100 105 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg  
115 120 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys  
130 135 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro  
145 150 155 160

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
165 170 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
180 185 190



Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr  
 195 200 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
 210 215 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His  
 225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
 245 250 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln  
 260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met  
 275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
 290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn  
 305 310 315 320

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu  
 325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile  
 340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln  
 355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 370 375

<210> 46  
 <211> 999  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 46  
 gcggccgcgc gtcgaccaag ggccccagcg tgttccccct ggccccctgc agccgcagca 60  
 ccagcgagag caccgcccgc ctgggctgcc tggatgaagga ctacttcccc gagcccgta 120  
 ccgtgagctg gaacagcggc gccctgacca gcggcgtagc caccttcccc gccgtgctgc 180  
 agagcagcgg cctgtactcc ctgagcagcg tggatgaccgt gccagcagc agcctgggca 240  
 ccaagacctc cacctgcaac gtggaccaca agcccagcaa caccaaggta gacaagcgcg 300  
 tggagagcaa gtacggcccc ccctgccccca gctgccccgc ccccgagttc ctgggcggcc 360  
 ccagcgtggt cctgttcccc cccaagccca aggacaccct gatgatcagc cgcacccccg 420  
 aggtgacctg cgtgggtggtg gacgtgagcc agggaggacc cgaggtagcag ttcaactggt 480  
 acgtggacgg cgtggagggtg cataacgcca agaccaagcc ccgcgaggag cagttcaaca 540  
 gcacctaccg cgtgggtgagc gtgctgaccg tgctgcacca ggactggctg aacggcaagg 600  
 agtacaagtg caagggtgtc aacaaggggc tgcccagcag catcgagaag accatcagca 660  
 aggccaaggc ccagccccgc gagccccagg tgtacaccct gccccccagc caggaggaga 720  
 tgaccaagaa ccagggtgagc ctgacctgcc tggatgaagg cttctacccc agcgacatcg 780  
 ccgtggagtg ggagagcaac ggccagcccc agaacaacta caagaccacc cccccctgc 840  
 tggacagcga cggcagcttc ttctgtaca gccgcctgac cgtggacaag agccgctggc 900  
 aggagggcaa cgtgttctcc tgctccgtga tgcatgaggc cctgcacaac cactacaccc 960  
 agaagagcct gagcctgagc ctgggcaagt gatagatct 999

<210> 47  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens

<400> 47

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
 1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr  
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys  
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro  
100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp  
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe  
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp  
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu  
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys  
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
 260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
 275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser  
 290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 305 310 315 320

Leu Ser Leu Ser Leu Gly Lys  
 325

<210> 48  
 <211> 337  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 48  
 gcggccgcac tgtggctgca ccattctgtct tcattcttccc gccattctgat gaggcagctta 60  
 agtccggaac cgccagcgtg gtgtgcctgc tgaacaactt ctacccccgc gaggccaagg 120  
 tgcagtggaa ggtggacaac gccctccaga gcggcaactc ccaggagagc gtgaccgagc 180  
 aggacagcaa ggacagcacc tacagcctga gcagcaccct gaccctgagc aaggccgact 240  
 acgagaagca caaggtgtac gcctgcgagg tgacccatca gggcctgagc agccccgtga 300  
 ccaagagctt caaccggggc gaggctagtg gagatct 337

<210> 49  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 49

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
 1 5 10 15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
 20 25 30

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
 35 40 45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
 50 55 60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
 65 70 75 80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
 85 90 95

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 100 105

<210> 50  
 <211> 346  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic

<400> 50  
 gcgggcgcac cgtcctaggt cagcccaagg cggcgcccag cgtgaccctg ttccccccca 60  
 gcagcgagga gctgcaggcc aacaaggcca ccctgggtgtg cctgatcagc gacttctacc 120  
 ccggggccgt gaccgtggcc tggaaggccg acagcagccc cgtgaaggcc ggcggtggaga 180  
 ccaccacccc cagcaagcag agcaacaaca agtacgccgc cagcagctac ctgagcctga 240  
 cccccgagca gtggaagagc caccgcagct acagctgcca ggtcaccac gagggcagca 300  
 ccgtggagaa gaccgtggcc cccaccgagt gcagctagtg agatct 346

<210> 51  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 51

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro  
 1 5 10 15

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
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Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
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Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu  
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